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RAW SEQUENCE LISTING              DATE: 02/14/2002
PATENT APPLICATION:  US/09/896,856   TIME: 19:05:04

Input Set : N:\Crf3\RULE60\09896856.txt
Output Set: N:\CRF3\02142002\I896856.raw
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ENTERED

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                    SEQUENCE LISTING
 3  (1) GENERAL INFORMATION:
 5       (i) APPLICANT: Baker, Joffre
 6                      Chien, Kenneth
 7                      King, Kathleen
 8                      Pennica, Diane
 9                      Wood, William
11      (ii) TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
13     (iii) NUMBER OF SEQUENCES: 8
15      (iv) CORRESPONDENCE ADDRESS:
16           (A) ADDRESSEE: Genentech, Inc.
17           (B) STREET: 460 Point San Bruno Blvd
18           (C) CITY: South San Francisco
19           (D) STATE: California
20           (E) COUNTRY: USA
21           (F) ZIP: 94080
23       (v) COMPUTER READABLE FORM:
24           (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
25           (B) COMPUTER: IBM PC compatible
26           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27           (D) SOFTWARE: WinPatin (Genentech)
29      (vi) CURRENT APPLICATION DATA:
C--> 30           (A) APPLICATION NUMBER: US/09/896,856
C--> 31           (B) FILING DATE: 29-Jun-2001
42           (C) CLASSIFICATION:
53     (vii) PRIOR APPLICATION DATA:
35           (A) APPLICATION NUMBER: US 08/733,850
36           (B) FILING DATE: 18-OCT-1996
40           (A) APPLICATION NUMBER: US 08/471,112
41           (B) FILING DATE: 06-JUN-1995
46           (A) APPLICATION NUMBER: 08/233,609
47           (B) FILING DATE: 25-APR-1994
50           (A) APPLICATION NUMBER: 08/286304
51           (B) FILING DATE: 05-AUG-1994
54           (A) APPLICATION NUMBER: 08/443129
55           (B) FILING DATE: 17-MAY-1995
57    (viii) ATTORNEY/AGENT INFORMATION:
58           (A) NAME: Conley, Deirdre L.
59           (B) REGISTRATION NUMBER: 36,487
60           (C) REFERENCE/DOCKET NUMBER: P0894P1D2C1
62      (ix) TELECOMMUNICATION INFORMATION:
63           (A) TELEPHONE: 415/225-2066
64           (B) TELEFAX: 415/952-9881
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RAW SEQUENCE LISTING   DATE: 02/14/2002
PATENT APPLICATION: US/09/896,856   TIME: 19:05:04

Input Set : N:\Crf3\RULE60\09896856.txt
Output Set: N:\CRF3\02142002\I896856.raw

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65          (C) TELEX: 910/371-7168
67 (2) INFORMATION FOR SEQ ID NO: 1:
69      (i) SEQUENCE CHARACTERISTICS:
70          (A) LENGTH: 1352 base pairs
71          (B) TYPE: Nucleic Acid
72          (C) STRANDEDNESS: Single
73          (D) TOPOLOGY: Linear
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
78  GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAGT CTGGAAGACC 50
80  ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC 100
82  CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAACT 150
84  TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTTGGG CTGCCGGGCT 200
86  TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC 250
88  CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT 300
90  GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCGGAGC 350
92  TGAACCCGCG CGCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC 400
94  CAGGTTCGGG CCCTGGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG 450
96  CGCTGCAGCC CGCGGGCCCG GGCCAGAGCC CGTCACCGTC GCCACCCTCT 500
98  TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC 550
100  CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT 600
102  GGGCCAGCTG GTGCCAGGGG GCGTCGCCTG AGAGTGAATA CTTTTTCTTG 650
104  TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT 700
106  CTGTGTCCTG TGTGTTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG 750
108  TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT 800
110  TTCTCGTTTT GTCTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC 850
112  TCTTTTTGTT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT 900
114  GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG 950
116  GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG 1000
118  CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT 1050
120  GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT 1100
122  TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTACTTGTCC CCTGGTGGCA 1150
124  AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC 1200
126  TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA 1250
128  GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT 1300
130  AATTTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA 1350
132  AA 1352
134 (2) INFORMATION FOR SEQ ID NO: 2:
136      (i) SEQUENCE CHARACTERISTICS:
137          (A) LENGTH: 1352 base pairs
138          (B) TYPE: Nucleic Acid
139          (C) STRANDEDNESS: Single
140          (D) TOPOLOGY: Linear
142      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
145  CCTATTCGGA CCCCGGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG 50
147  TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG 100
149  GCGGTCTGTG TGTTGGAACG GGCGGAGGAC TGGTTTATAC GTCTTGTTGA 150
151  AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA 200
153  AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG 250
155  GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCCTAC GTCGGCGGGA 300
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157  CTCACACGAC GGGCGCGACA ACCTACGGCA GGCGGCGGCG GTCCGCCTCG 350
159  ACTTGGGCGC GCGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG 400
161  GTCCAAGCCC GGGACCCGCG GCGCCACCTC TGTCACGACC GGCGCGACCC 450
163  GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CGGTGGGAGA 500
165  AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG 550
167  GTGCACACGC CGGAGATACC GCTCACCCAC TCGGCGTGTC TCCCGCTGGA 600
169  CCCGGTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAGAAC 650
171  ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA 700
173  GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC 750
175  AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA 800
177  AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG 850
179  AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA 900
181  CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC 950
183  CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC 1000
185  GGAGGCTGAG GGTTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA 1050
187  CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAAG AGGGAAGTCA 1100
189  AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT 1150
191  TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG 1200
193  AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT 1250
195  CTCTCTTTCC GTCTTTTTGT AGAAATTTCT CAAAATAAAC TCTTATTTAA 1300
197  TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTTGAA AATACTTTTT 1350
199  TT 1352
201  (2) INFORMATION FOR SEQ ID NO: 3:
203      (i) SEQUENCE CHARACTERISTICS:
204          (A) LENGTH: 203 amino acids
205          (B) TYPE: Amino Acid
206          (D) TOPOLOGY: Linear
208      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
210  Met Ser Gln Arg Glu Gly Ser Leu Glu Asp His Gln Thr Asp Ser
211   1               5                  10                  15
213  Ser Ile Ser Phe Leu Pro His Leu Glu Ala Lys Ile Arg Gln Thr
214                  20                  25                  30
216  His Asn Leu Ala Arg Leu Leu Thr Lys Tyr Ala Glu Gln Leu Leu
217                  35                  40                  45
219  Glu Glu Tyr Val Gln Gln Gln Gly Glu Pro Phe Gly Leu Pro Gly
220                  50                  55                  60
222  Phe Ser Pro Pro Arg Leu Pro Leu Ala Gly Leu Ser Gly Pro Ala
223                  65                  70                  75
225  Pro Ser His Ala Gly Leu Pro Val Ser Glu Arg Leu Arg Gln Asp
226                  80                  85                  90
228  Ala Ala Ala Leu Ser Val Leu Pro Ala Leu Leu Asp Ala Val Arg
229                  95                  100                 105
231  Arg Arg Gln Ala Glu Leu Asn Pro Arg Ala Pro Arg Leu Leu Arg
232                  110                 115                 120
234  Ser Leu Glu Asp Ala Ala Arg Gln Val Arg Ala Leu Gly Ala Ala
235                  125                 130                 135
237  Val Glu Thr Val Leu Ala Ala Leu Gly Ala Ala Ala Arg Gly Pro
238                  140                 145                 150
240  Gly Pro Glu Pro Val Thr Val Ala Thr Leu Phe Thr Ala Asn Ser
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RAW SEQUENCE LISTING
DATE: 02/14/2002
PATENT APPLICATION: US/09/896,856
TIME: 19:05:04

Input Set : N:\Crf3\RULE60\09896856.txt
Output Set: N:\CRF3\02142002\I896856.raw

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241                     155              160              165
243    Thr Ala Gly Ile Phe Ser Ala Lys Val Leu Gly Phe His Val Cys
244                     170              175              180
246    Gly Leu Tyr Gly Glu Trp Val Ser Arg Thr Glu Gly Asp Leu Gly
247                     185              190              195
249    Gln Leu Val Pro Gly Gly Val Ala
250                     200         203
252  (2) INFORMATION FOR SEQ ID NO: 4:
254       (i) SEQUENCE CHARACTERISTICS:
255            (A) LENGTH: 200 amino acids
256            (B) TYPE: Amino Acid
257            (D) TOPOLOGY: Linear
259      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
261    Met Ala Phe Thr Glu His Ser Pro Leu Thr Pro His Arg Arg Asp
262     1               5               10               15
264    Leu Cys Ser Arg Ser Ile Trp Leu Ala Arg Lys Ile Arg Ser Asp
265                     20              25               30
267    Leu Thr Ala Leu Thr Glu Ser Tyr Val Lys His Gln Gly Leu Asn
268                     35              40               45
270    Lys Asn Ile Asn Leu Asp Ser Ala Asp Gly Met Pro Val Ala Ser
271                     50              55               60
273    Thr Asp Gln Trp Ser Glu Leu Thr Glu Ala Glu Arg Leu Gln Glu
274                     65              70               75
276    Asn Leu Gln Ala Tyr Arg Thr Phe His Val Leu Leu Ala Arg Leu
277                     80              85               90
279    Leu Glu Asp Gln Gln Val His Phe Thr Pro Thr Glu Gly Asp Phe
280                     95              100              105
282    His Gln Ala Ile His Thr Leu Leu Leu Gln Val Ala Ala Phe Ala
283                     110             115              120
285    Tyr Gln Ile Glu Glu Leu Met Ile Leu Leu Glu Tyr Lys Ile Pro
286                     125             130              135
288    Arg Asn Glu Ala Asp Gly Met Pro Ile Asn Val Gly Asp Gly Gly
289                     140             145              150
291    Leu Phe Glu Lys Lys Leu Trp Gly Leu Lys Val Leu Gln Glu Leu
292                     155             160              165
294    Ser Gln Trp Thr Val Arg Ser Ile His Asp Leu Arg Phe Ile Ser
295                     170             175              180
297    Ser His Gln Thr Gly Ile Pro Ala Arg Gly Ser His Tyr Ile Ala
298                     185             190              195
300    Asn Asn Lys Lys Met
301                     200
303  (2) INFORMATION FOR SEQ ID NO: 5:
305       (i) SEQUENCE CHARACTERISTICS:
306            (A) LENGTH: 50 base pairs
307            (B) TYPE: Nucleic Acid
308            (C) STRANDEDNESS: Single
309            (D) TOPOLOGY: Linear
311      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
314    GCGGCCGCGA GCTCGAATTC TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 50
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316 (2) INFORMATION FOR SEQ ID NO: 6:
318      (i) SEQUENCE CHARACTERISTICS:
319          (A) LENGTH: 1018 base pairs
320          (B) TYPE: Nucleic Acid
321          (C) STRANDEDNESS: Single
322          (D) TOPOLOGY: Linear
324     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
327 GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA 50
329 AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT 100
331 GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT 150
333 ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC 200
335 GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC 250
337 CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG 300
339 ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC 350
341 CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCTGGA 400
343 GGACGCGGCG CGCCAGGCCC GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC 450
345 TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCCGGGCCGA GCCCCCCGCC 500
347 GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT 550
349 GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG 600
351 GCGACCTGGG CCAGCTGCTG CCCGGGGGGCT CGGCCTGAGC GCCGCGGGGC 650
353 AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT 700
355 GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC 750
357 ATTGCCTCGG CCTTCTTTGC TTTTTGTGGG GGAGAGGGGA GGGGACGGGC 800
359 AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC 850
361 AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC 900
363 AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA 950
365 TTTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAACT 1000
367 CCGGGGCTCA AGCGATCC 1018
369 (2) INFORMATION FOR SEQ ID NO: 7:
371      (i) SEQUENCE CHARACTERISTICS:
372          (A) LENGTH: 1018 base pairs
373          (B) TYPE: Nucleic Acid
374          (C) STRANDEDNESS: Single
375          (D) TOPOLOGY: Linear
377     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
380 CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT 50
382 TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA 100
384 CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA 150
386 TGCGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG 200
388 CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG 250
390 GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC 300
392 TGCGCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG 350
394 GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT 400
396 CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG 450
398 ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGCCCGGCT CGGGGGGCGG 500
400 CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCCACGA 550
402 CCCCGAGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC 600
404 CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG 650
406 TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA 700
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VERIFICATION SUMMARY   DATE: 02/14/2002
PATENT APPLICATION: US/09/896,856   TIME: 19:05:05

Input Set : **N:\Crf3\RULE60\09896856.txt**
Output Set: **N:\CRF3\02142002\I896856.raw**

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]